



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/780,113A

Source: 1645

Date Processed by STIC: 5/30/2001

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JUN 1 2 2001

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

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JUN 12 2001

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Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/780/113A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
 Wrapped Aminos
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
 Numbering
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
 "bug"
- 7 Skipped Sequences Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
 (OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped
- Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
 (NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
 (NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
 Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
 "bug"

1645

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/780,113A

DATE: 05/30/2001
TIME: 11:01:31

Input Set : A:\506812000120.txt
Output Set : C:\CRF3\05302001\I780113A.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: TYRRELL, JOHN V.
4 BERGQUIST, PATRICIA R.
5 BERGQUIST, PETER L.
6 SCHOLIN, CHRISTOPHER A.
8 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING RAPIDOPHYTES
10 <130> FILE REFERENCE: 50681200121
12 <140> CURRENT APPLICATION NUMBER: 09/780,113A
13 <141> CURRENT FILING DATE: 2001-02-09
15 <150> PRIOR APPLICATION NUMBER: 09/596,136
W--> 16 60/141,362 *add 1/507*
18 <151> PRIOR FILING DATE: 2000-06-16
W--> 19 1999-06-28 *1/517*
21 ~~160~~ NUMBER OF SEQ ID NOS: 30
23 <170> SOFTWARE: PatentIn Ver. 2.1

*do not separate application
numbers and their filing
dates - group them
together*

*E.S. 1/507 60/141,362
1/517 1999-06-28*

ERRORED SEQUENCES

259 <210> SEQ ID NO: 20
260 <211> LENGTH: 25
261 <212> TYPE: DNA
262 <213> ORGANISM: Artificial Sequence
264 <220> FEATURE:
265 <223> OTHER INFORMATION: Description of Artificial Sequence: Artificial
probe
E--> 267 <400> SEQUENCE: (25)20
C--> 268 ~~tcacatctttcc~~ ~~ctcacgggtac~~ ~~ttgtt~~ 25

oligonucleotide

olignucleotide

(global error)

*when using raw
sequence files
format, use
lower-case*

*letters for all
bases (Please
correct
this global error)*

All following page for more errors

2

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/780,113A

DATE: 06/08/2001
TIME: 18:21:18

Input Set : A:\Pto.amc
Output Set : N:\CRF3\06082001\I780113A.raw

295 <210> SEQ ID NO: 23
296 <211> LENGTH: 23
297 <212> TYPE: DNA
298 <213> ORGANISM: Artificial Sequence
300 <220> FEATURE:
301 <223> OTHER INFORMATION: Description of -Artificial Sequence:
303 <400> SEQUENCE: 23
C--> 304 agagtagctg agcacgcac tct
307 <210> SEQ ID NO: 24
308 <211> LENGTH: 687
309 <212> TYPE: DNA
310 <213> ORGANISM: Chattonella antiqua
312 <400> SEQUENCE: 24
C--> 313 ttcttgaagc ggaggaaaag aaccaactcg gattccctag taacggcgag tgaagcggga 60
314 agagctcatg ttgtaaatct ggatgaggat tctctgtccc gaattgtagt cttagagatgc 120
315 gtgtctcagct actctccagg gctaagctctg ttgtgaaaag acagcatcat ggacgggtgat 180
316 aatccggttc ttgcttggga ttgtgtagcg tcttgagccg tctccaacga gtccagttgc 240
317 ttgggattgc agctctcaagc ggggtggtaaa ttccatctaa agctaaatat tgggtgggaga 300
318 ccgatagcga acaagtaccg tgagggaagaa atgaaaagaa ctttgaaaag agagttaaat 360
319 agtacctgaa actgctgaaa gggaagcgaa tgaagtcagt gttgctcttt gttctctgca 420
320 tctctcctgc ggggattgtg tatcgaggac ttgagcttg tcaagatgag tctctgcgcg 480
321 cgggatatgg ttgtgagct ggatgctctc gctgaactca cctctctgt cgtgcttg 540
322 actgaggttc catcttgcg ttgctgtgt gttactctcc tgttctgtt tctgtctac 600
323 tgtctgcagt gttcggttgc agtgattgga ctgtgcaagt tatgcatgca aggtcaggat 660
324 cctgacgaat ggcctttata acccgaa 687
327 <210> SEQ ID NO: 25
328 <211> LENGTH: 681
329 <212> TYPE: DNA
330 <213> ORGANISM: Chattonella subsalsa
332 <400> SEQUENCE: 25
C--> 333 gggaggaaaa agaaccaact cggattccct agtaacggcg agtgaagcgg gaagagctca 60
334 tgttgtaaat ctggatgagg gttcctcgto cgaatttga gtctagagat cgggtgctcag 120
335 ctactctcca gggctaagtc gtgttgtgaa agacagtgto atgacgggtg ataaccgggt 180
336 tcttgccctg gatgtttag cgttttgagc cgtcctcaac gagtgcagtt gcttgggatt 240
337 gcaagctctaa gtgggtggta aattccaact aaagctaaat attgtgggga gaccgatagc 300
338 gaacaagtac cgtgaggaaa agatgaaaaa aactttgaaa agagagttaa atagtacctg 360
339 aaactgtcta aagggaagcg aatgaagtca gtgttgcct ttgtgctctg catcctccct 420
340 ggggggattg tgtatcgagg actttgagct tgtcaggatg agttctctgc cgcgggatat 480
341 gttttgtatg ctggatgctt ttgcggaac atacattctc tgtctgtgct tggactgaag 540
342 tcccatcttg ccgttgctgt tgcgttctcc tcccgttgct gctctgttcc tactgcttgc 600
343 agtgctcagt tgcagtagtt ggactgtgct tattatgcat gcaaggtcag gatcctgacg 660
344 aatggccttta ttcaccogca a
347 <210> SEQ ID NO: 26
348 <211> LENGTH: 703
349 <212> TYPE: DNA
350 <213> ORGANISM: Fibrocapsa japonica
352 <400> SEQUENCE: 26
C--> 353 cagagggaaaa gaaccaactc ggattcccta gtaacggcga gtgaagcggg aacagctcat 60
354 gatgtaaatc tgggtgcagct tgcgttacc cgaattgtag tctacagaag cgtgtccagc 120

invalid - give source
Artificial
of genetic material.
See circled portion of item 11 on Envs summary sheet.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/780,113A

DATE: 05/30/2001

TIME: 11:01:32

Input Set : A:\506812000120.txt

Output Set : C:\CRF3\05302001\I780113A.raw

L:16 M:259 W: Allowed number of lines exceeded, <150> PRIOR APPLICATION NUMBER:
L:19 M:259 W: Allowed number of lines exceeded, <151> PRIOR FILING DATE:
L:37 M:112 C: (48) String data converted to lower case,
L:52 M:112 C: (48) String data converted to lower case,
L:64 M:112 C: (48) String data converted to lower case,
L:76 M:112 C: (48) String data converted to lower case,
L:88 M:112 C: (48) String data converted to lower case,
L:100 M:112 C: (48) String data converted to lower case,
L:112 M:112 C: (48) String data converted to lower case,
L:124 M:112 C: (48) String data converted to lower case,
L:136 M:112 C: (48) String data converted to lower case,
L:148 M:112 C: (48) String data converted to lower case,
L:160 M:112 C: (48) String data converted to lower case,
L:172 M:112 C: (48) String data converted to lower case,
L:184 M:112 C: (48) String data converted to lower case,
L:196 M:112 C: (48) String data converted to lower case,
L:208 M:112 C: (48) String data converted to lower case,
L:220 M:112 C: (48) String data converted to lower case,
L:232 M:112 C: (48) String data converted to lower case,
L:244 M:112 C: (48) String data converted to lower case,
L:256 M:112 C: (48) String data converted to lower case,
L:267 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:20 differs:25
L:268 M:112 C: (48) String data converted to lower case,
L:280 M:112 C: (48) String data converted to lower case,
L:292 M:112 C: (48) String data converted to lower case,
L:304 M:112 C: (48) String data converted to lower case,
L:313 M:112 C: (48) String data converted to lower case,
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L:340 M:112 C: (48) String data converted to lower case,
L:341 M:112 C: (48) String data converted to lower case,
L:342 M:112 C: (48) String data converted to lower case,

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/780,113A

DATE: 05/30/2001

TIME: 11:01:32

Input Set : A:\506812000120.txt

Output Set : C:\CRF3\05302001\I780113A.raw

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L:403 M:112 C: (48) String data converted to lower case,
L:404 M:112 C: (48) String data converted to lower case,
L:418 M:112 C: (48) String data converted to lower case,
L:430 M:112 C: (48) String data converted to lower case,